

DMCI0099.ST25.txt
SEQUENCE LISTING

<110> Havkin-Frenkel, Daphna
Podstolski, Andrzej
Dixon, Richard A.

<120> Vanillin Biosynthetic Pathway Enzyme From Vanilla Planifolia

<130> DMCI0099

<150> 09/462,576
<151> 2000-05-22

<150> PCT/US98/14895
<151> 1998-07-15

<150> 60/052,604
<151> 1997-07-15

<150> 60/272,415
<151> 2001-02-28

<160> 25

<170> PatentIn version 3.1

<210> 1
<211> 1071
<212> DNA
<213> Vanilla planifolia

<400> 1
atggcagcta agtcctctt cttcctactc ttccctggctc ccgcctctc cgtcgcgctc 60
gccggtttcg aagaagacaa tccaatccgg tccgttacac aaaggcctga ctgcatttag 120
cctgccatcc tcggcgctt tggcagttgc cgccacgcct tccacttcgc acggttcgcc 180
cgcaggtacg ggaagagcta cggatcggag gaggagatca agaagagggtt cggatcttc 240
gtggagaatc tagcgtttat ccggtccact aatcggagg atctgtcgta taccctagga 300
atcaaccaat tcgcccacct gacctggag gaattccgga ccaatgcct tggtcgccg 360
cagaactgct cggcgactgc gcatggaaac caccggtttgc tcgatggcgt gcttcctgt 420
acgagggatt ggagggagca agggatagtg agccctgtaa aggaccaagg aagctgtgga 480
tcttgctgga ct当地cgtac tactggagca ctagaggctg catatacaca gctaactgga 540
aagagcacat cattatctga acagcaactt gtggactgtg cctcagcatt caataacttt 600
ggatgcaatg gaggtttgcc ttcccaagcc tttgaatacg ttaagtacaa tggaggcatc 660
gacacagaac agacttatcc ataccttggt gtcaatggta tctgcaactt caagcaggag 720
aatgttggtg tcaaggtcat tgattcgata aacatcaccc tgggtgctga ggatgagttg 780
aagcatgcag tggcgttgcgt gcgtccagtt agcgttgcatt ttgaggttgt gaaaggttc 840
aatctgtaca agaaaagggtgt atacagcagt gacacctgtg gaagagatcc aatggatgtg 900
aaccacgcag ttcttgccgt cggttatgga gtcgaggacg ggattcctta ttggctcattc 960

DMCI0099.ST25.txt

aagaactcat ggggtacaaa ttggggtgac aatggctact ttaagatgga actcggcaag 1020
 aacatgtgtg gtgttgcaac ttgcgcac tatccattg tggctgtgta g 1071

<210> 2
 <211> 352
 <212> PRT
 <213> Vanilla planifolia

<400> 2

Met Ala Ala Lys Leu Leu Phe Phe Leu Leu Phe Leu Val Ser Ala Leu
 1 5 10 15

Ser Val Ala Leu Ala Gly Phe Glu Glu Asp Asn Pro Ile Arg Ser Val
 20 25 30

Thr Gln Arg Pro Asp Ser Ile Glu Pro Ala Ile Leu Gly Val Leu Gly
 35 40 45

Ser Cys Arg His Ala Phe His Phe Ala Arg Phe Ala Arg Arg Tyr Gly
 50 55 60

Lys Ser Tyr Gly Ser Glu Glu Glu Ile Lys Lys Arg Phe Gly Ile Phe
 65 70 75 80

Val Glu Asn Leu Ala Phe Ile Arg Ser Thr Asn Arg Lys Asp Leu Ser
 85 90 95

Tyr Thr Leu Gly Ile Asn Gln Phe Ala Asp Leu Thr Trp Glu Glu Phe
 100 105 110

Arg Thr Asn Arg Leu Gly Ala Ala Gln Asn Cys Ser Ala Thr Ala His
 115 120 125

Gly Asn His Arg Phe Val Asp Gly Val Leu Pro Val Thr Arg Asp Trp
 130 135 140

Arg Glu Gln Gly Ile Val Ser Pro Val Lys Asp Gln Gly Ser Cys Gly
 145 150 155 160

Ser Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala Ala Tyr Thr Gln
 165 170 175

Leu Thr Gly Ser Thr Leu Ser Glu Gln Gln Leu Val Asp Cys Ala Ser
 180 185 190

Ala Phe Asn Asn Phe Gly Cys Gly Gly Leu Pro Ser Gln Ala Phe Glu
 195 200 205

DMCI0099.ST25.txt

Tyr Val Lys Tyr Asn Gly Gly Ile Asp Thr Glu Gln Thr Tyr Pro Tyr
210 215 220

Leu Gly Val Met Gly Ile Cys Asn Phe Lys Gln Glu Asn Val Gly Val
225 230 235 240

Lys Val Ile Asp Ser Ile Asn Ile Thr Leu Gly Ala Glu Asp Glu Leu
245 250 255

Lys His Ala Val Gly Leu Val Arg Pro Val Ser Val Ala Phe Glu Val
260 265 270

Val Lys Gly Phe Asn Leu Tyr Lys Lys Gly Val Tyr Ser Ser Asp Thr
275 280 285

Cys Gly Arg Asp Pro Met Asp Val Asn His Ala Val Leu Ala Val Gly
290 295 300

Tyr Gly Val Glu Asp Gly Ile Pro Tyr Trp Leu Ile Lys Asn Ser Trp
305 310 315 320

Gly Thr Asn Trp Gly Asp Asn Gly Tyr Phe Lys Met Glu Leu Gly Lys
325 330 335

Asn Met Cys Gly Val Ala Thr Cys Ala Ser Tyr Pro Ile Val Ala Val
340 345 350

<210> 3<211> 7<212> PRT<213> Artificial Sequence<220><223> Novel Sequence

<400> 3

Gly Val Leu Pro Val Thr Arg
1 5

<210> 4
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 4

Asn Ser Trp Gly Thr Asn Trp Gly Asp Asn Gly Tyr Phe
1 5 10

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

DMCI0099.ST25.txt

<223> Novel Sequence

<400> 5

Gly Phe Asn Leu Tyr Lys
1 5

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 6

Gln Gly Ile Val Ser Pro Val Lys
1 5

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 1a 5

<220>

<221> misc_feature

<222> (3)..(3)

<223> N= Inosine

<220>

<221> misc_feature

<222> (6)..(6)

<223> N= Inosine

<220>

<221> misc_feature

<222> (9)..(9)

<223> N= Inosine

<220>

<221> misc_feature

<222> (12)..(12)

<223> N= Inosine

<220>

<221> misc_feature

<222> (15)..(15)

<223> N= I

<220>

<221> misc_feature

<222> (18)..(18)

<223> N= I

<400> 7

ggngtnc tnc cngtnacncg

20

DMCI0099.ST25.txt

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer 1a 5

<220>
<221> misc_feature
<222> (3)..(3)
<223> N= Inosine

<220>
<221> misc_feature
<222> (6)..(6)
<223> N= Inosine

<220>
<221> misc_feature
<222> (9)..(9)
<223> N= Inosine

<220>
<221> misc_feature
<222> (12)..(12)
<223> N= Inosine

<220>
<221> misc_feature
<222> (15)..(15)
<223> N= Inosine

<220>
<221> misc_feature
<222> (18)..(18)
<223> N= Inosine

<400> 8
cgngtnacng gnagnacncc

20

<210> 9
<211> 41
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer 2a 5

<220>
<221> misc_feature
<222> (3)..(3)
<223> N= t or c

<220>
<221> misc_feature
<222> (6)..(6)
<223> N= Inosine

<220>

DMCI0099.ST25.txt

<221> misc_feature
 <222> (12)..(12)
 <223> N= Inosine

 <220>
 <221> misc_feature
 <222> (15)..(15)
 <223> N= Inosine

 <220>
 <221> misc_feature
 <222> (18)..(18)
 <223> N= t or c

 <220>
 <221> misc_feature
 <222> (24)..(24)
 <223> N= Inosine

 <220>
 <221> misc_feature
 <222> (27)..(27)
 <223> N= t or c

 <220>
 <221> misc_feature
 <222> (30)..(30)
 <223> N= t or c

 <220>
 <221> misc_feature
 <222> (33)..(33)
 <223> N= Inosine

 <220>
 <221> misc_feature
 <222> (36)..(36)
 <223> N= t or c

 <220>
 <221> misc_feature
 <222> (39)..(39)
 <223> N= t or c

 <400> 9
 aantcntggg gnacnaantg gggnganaan ggntanttna a

41

<210> 10
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer 2b 5

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> N= c or t

<220>
 <221> misc_feature

DMCI0099.ST25.txt

```

<222> (4)..(4)
<223> N= g or a

<220>
<221> misc_feature
<222> (7)..(7)
<223> N= g or a

<220>
<221> misc_feature
<222> (10)..(10)
<223> N= Inosine

<220>
<221> misc_feature
<222> (13)..(13)
<223> N= g or a

<220>
<221> misc_feature
<222> (16)..(16)
<223> N= g or a

#<220>
#<221> misc_feature
#<222> (19)..(19)
#<223> N= Inosine

<220>
<221> misc_feature
<222> (25)..(25)
<223> N= g or a

#<220>
#<221> misc_feature
#<222> (28)..(28)
#<223> N= Inosine

<220>
<221> misc_feature
<222> (31)..(31)
<223> N= Inosine

<220>
<221> misc_feature
<222> (37)..(37)
<223> N= Inosine

<220>
<221> misc_feature
<222> (40)..(40)
<223> N= g or a

<400> 10
nttnaantan ccntntcnc cccantngt nccccangan tt

```

42

```

<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

```

```
<220>
```

DMCI0099.ST25.txt

<223> Primer 3a 5

<220>
<221> misc_feature
<222> (3)..(3)
<223> N= Inosine

<220>
<221> misc_feature
<222> (6)..(6)
<223> N= t or c

<220>
<221> misc_feature
<222> (9)..(9)
<223> N= t or c

<220>
<221> misc_feature
<222> (12)..(12)
<223> N= Inosine

<220>
<221> misc_feature
<222> (15)..(15)
<223> N= t or c

<400> 11
ggnttnaanc tntanaa

17

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer 3b5

<220>
<221> misc_feature
<222> (1)..(1)
<223> N= c or t

<220>
<221> misc_feature
<222> (4)..(4)
<223> N= g or a

<220>
<221> misc_feature
<222> (7)..(7)
<223> N= Inosine

<220>
<221> misc_feature
<222> (10)..(10)
<223> N= g or a

<220>
<221> misc_feature
<222> (13)..(13)
<223> N= g or a

DMCI0099.ST25.txt

<220>
<221> misc_feature
<222> (16)..(16)
<223> N= Inosine

<400> 12
nttntanagn ttnaancc 18

<210> 13
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> 4HBS P1a

<400> 13
ggaattccat atggcagcta agtcctctt c 31

~~1.0000000000000001~~
<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> 4HBS P1b

<400> 14
cgcgatatccc tacacagcca caatggg 27

~~1.0000000000000001~~
<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> 4HBS P2a

<400> 15
cccatatgct tcctgttaacg agggattgg 29

~~1.0000000000000001~~
<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> 4HBS P3b

<400> 16
ccccctcgaga tggcagctaa gctcctttc 30

~~1.0000000000000001~~
<210> 17
<211> 28

DMCI0099.ST25.txt

<212> DNA
<213> Artificial Sequence
<220>
<223> 4HBS P3b
<400> 17
ccccactagt ctacacagcc acaatggg 28

<210> 18
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligo 1
<400> 18
gtatctgagc tcaaaaatgg cagctaagct cctc 34

<210> 19
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligo 2
<400> 19
catagaggat ccctacacag ccacaatggg ataa 34

<210> 20
<211> 360
<212> PRT
<213> Arabidopsis thaliana
<400> 20

Met Ser Ala Lys Thr Ile Leu Ser Ser Val Val Leu Val Val Leu Val
1 5 10 15

Ala Ala Ser Ala Ala Asn Ile Gly Phe Asp Glu Ser Asn Pro Ile
20 25 30

Arg Met Val Ser Asp Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln
35 40 45

Ile Leu Gly Gln Ser Arg His Val Leu Ser Phe Ala Arg Phe Thr His
50 55 60

Arg Tyr Gly Lys Lys Tyr Gln Asn Val Glu Glu Met Lys Leu Arg Phe
65 70 75 80

DMCI0099.ST25.txt

Ser Ile Phe Lys Glu Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys
85 90 95

Gly Leu Ser Tyr Lys Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp
100 105 110

Gln Glu Phe Gln Arg Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala
115 120 125

Thr Leu Lys Gly Ser His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr
130 135 140

Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly
145 150 155 160

Gly Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala
165 170 175

Ala Tyr His Gln Ala Phe Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu
180 185 190

Gln Gln Leu Val Asp Cys Ala Gly Ala Phe Asn Asn Tyr Gly Cys Asn
195 200 205

Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly
210 215 220

Leu Asp Thr Glu Lys Ala Tyr Pro Tyr Thr Gly Lys Asp Glu Thr Cys
225 230 235 240

Lys Phe Ser Ala Glu Asn Val Gly Val Gln Val Leu Asn Ser Val Ser
245 250 255

Ile Thr Leu Gly Ala Glu Asp Glu Leu Lys His Ala Val Gly Leu Val
260 265 270

Arg Pro Val Ser Ile Ala Phe Glu Val Ile His Ser Phe Arg Leu Tyr
275 280 285

Lys Ser Gly Val Tyr Thr Asp Ser His Cys Gly Ser Thr Pro Met Asp
290 295 300

Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asp Gly Val
305 310 315 320

Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly Asp Lys
325 330 335

DMCI0099.ST25.txt

Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Gly Ile Ala Thr
 340 345 350

Cys Ala Ser Tyr Pro Val Val Ala
 355 360

<210> 21
 <211> 362
 <212> PRT
 <213> Hordeum vulgare

<400> 21

Met Ala His Ala Arg Val Leu Leu Leu Ala Leu Ala Val Leu Ala Thr
 1 5 10 15

Ala Ala Val Ala Val Ala Ser Ser Ser Ser Phe Ala Asp Ser Asn Pro
 20 25 30

Ile Arg Pro Val Thr Asp Arg Ala Ala Ser Thr Leu Glu Ser Ala Val
 35 40 45

Leu Gly Ala Leu Gly Arg Thr Arg His Ala Leu Arg Phe Ala Arg Phe
 50 55 60

Ala Val Arg Tyr Gly Lys Ser Tyr Glu Ser Ala Ala Glu Val Arg Arg
 65 70 75 80

Arg Phe Arg Ile Phe Ser Glu Ser Leu Glu Glu Val Arg Ser Thr Asn
 85 90 95

Arg Lys Gly Leu Pro Tyr Arg Leu Gly Ile Asn Arg Phe Ser Asp Met
 100 105 110

Ser Trp Glu Glu Phe Gln Ala Thr Arg Leu Gly Ala Ala Gln Thr Cys
 115 120 125

Ser Ala Thr Lys Gly Asn His Leu Met Arg Asp Ala Ala Ala Leu Pro
 130 135 140

Glu Thr Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asn
 145 150 155 160

Gln Ala His Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu
 165 170 175

Glu Ala Ala Tyr Thr Gln Ala Thr Gly Lys Asn Ile Ser Leu Ser Glu
 180 185 190

Gln Gln Leu Val Asp Cys Ala Gly Gly Phe Asn Asn Phe Gly Cys Asn
 Page 12

DMCI0099.ST25.txt

195

200

205

Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Tyr Asn Gly Gly
 210 215 220

Ile Asp Thr Glu Glu Ser Tyr Pro Tyr Lys Gly Val Asn Gly Val Cys
 225 230 235 240

His Tyr Lys Ala Glu Asn Ala Ala Val Gln Val Leu Asp Ser Val Asn
 245 250 255

Ile Thr Leu Asn Ala Glu Asp Glu Leu Lys Asn Ala Val Gly Leu Val
 260 265 270

Arg Pro Val Ser Val Ala Ala Phe Gln Val Ile Asp Gly Phe Arg Gln
 275 280 285

Tyr Lys Ser Gly Val Tyr Thr Ser Asp His Cys Gly Thr Thr Pro Asp
 290 295 300

Asp Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asn Gly
 305 310 315 320

Val Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly Asp
 325 330 335

Asn Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Ala Ile Ala
 340 345 350

Thr Cys Ala Ser Tyr Pro Val Val Ala Ala
 355 360

<210> 22
 <211> 360
 <212> PRT
 <213> Nicotiana tabaccum

<400> 22

Met Ser Arg Phe Ser Leu Leu Leu Ala Leu Val Val Ala Gly Gly Leu
 1 5 10 15

Phe Ala Ser Ala Leu Ala Gly Pro Ala Thr Phe Ala Asp Glu Asn Pro
 20 25 30

Ile Arg Gln Val Val Ser Asp Gly Leu His Glu Leu Glu Asn Ala Ile
 35 40 45

Leu Gln Val Val Gly Lys Thr Arg His Ala Leu Ser Phe Ala Arg Phe
 50 55 60

DMCI0099.ST25.txt

Ala His Arg Tyr Gly Lys Arg Tyr Glu Ser Val Glu Glu Ile Lys Gln
65 70 75 80

Arg Phe Glu Val Phe Leu Asp Asn Leu Lys Met Ile Arg Ser His Asn
85 90 95

Lys Lys Gly Leu Ser Tyr Lys Leu Gly Val Asn Glu Phe Thr Asp Leu
100 105 110

Thr Trp Asp Glu Phe Arg Arg Asp Arg Leu Gly Ala Ala Gln Asn Cys
115 120 125

Ser Ala Thr Thr Lys Gly Asn Leu Lys Val Thr Asn Val Val Leu Pro
130 135 140

Glu Thr Lys Asp Trp Arg Glu Ala Gly Ile Val Ser Pro Val Lys Asn
145 150 155 160

Gln Gly Lys Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu
165 170 175

Glu Ala Ala Tyr Ser Gln Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu
180 185 190

Gln Gln Leu Val Asp Cys Ala Gly Ala Phe Asn Asn Phe Gly Cys Asn
195 200 205

Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly
210 215 220

Leu Asp Thr Glu Glu Ala Tyr Pro Tyr Thr Gly Lys Asn Gly Leu Cys
225 230 235 240

Lys Phe Ser Ser Glu Asn Val Gly Val Lys Val Ile Asp Ser Val Asn
245 250 255

Ile Thr Leu Gly Ala Glu Asp Glu Leu Lys Tyr Ala Val Ala Leu Val
260 265 270

Arg Pro Val Ser Ile Ala Phe Glu Val Ile Lys Gly Phe Lys Gln Tyr
275 280 285

Lys Ser Gly Val Tyr Thr Ser Thr Glu Cys Gly Asn Thr Pro Met Asp
290 295 300

Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asp Gly Val
305 310 315 320

DMCI0099.ST25.txt

Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly Asp Glu
325 330 335

Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Gly Val Ala Thr
340 345 350

Cys Ala Ser Tyr Pro Val Val Ala
355 360

<210> 23
<211> 360
<212> PRT
<213> Zea mays

<400> 23

Met Ala Pro Arg Arg Leu Leu Val Leu Ala Val Val Ala Leu Ala Ala
1 5 10 15

Thr Ala Ala Ala Ala Asn Ser Gly Phe Ala Asp Ser Asn Pro Ile Arg
20 25 30

Pro Val Thr Asp Arg Ala Ala Ser Ala Leu Glu Ser Thr Val Phe Ala
35 40 45

Ala Leu Gly Arg Thr Arg Asp Ala Leu Arg Phe Ala Arg Phe Ala Val
50 55 60

Arg Tyr Gly Lys Ser Tyr Glu Ser Ala Ala Glu Val His Lys Arg Phe
65 70 75 80

Arg Ile Phe Ser Glu Ser Leu Gln Leu Val Arg Ser Thr Asn Arg Lys
85 90 95

Gly Leu Ser Tyr Arg Leu Gly Ile Asn Arg Phe Ala Asp Met Ser Trp
100 105 110

Glu Glu Phe Arg Ala Thr Arg Leu Gly Ala Ala Gln Asn Cys Ser Ala
115 120 125

Thr Leu Thr Gly Asn His Arg Met Arg Ala Ala Ala Val Ala Leu Pro
130 135 140

Glu Thr Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asn
145 150 155 160

Gln Gly His Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu
165 170 175

DMCI0099.ST25.txt

Glu Ala Ala Tyr Thr Gln Ala Thr Gly Lys Pro Ile Ser Leu Ser Glu
180 185 190

Gln Gln Leu Val Asp Cys Gly Leu Ala Phe Asn Asn Phe Gly Cys Asn
195 200 205

Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Tyr Asn Gly Gly
210 215 220

Leu Asp Thr Glu Glu Ser Tyr Pro Tyr Gln Gly Val Asn Gly Ile Ser
225 230 235 240

Lys Phe Lys Asn Glu Asn Val Gly Val Lys Val Leu Asp Ser Val Asn
245 250 255

Ile Thr Leu Gly Ala Glu Asp Glu Leu Lys Asp Ala Val Gly Leu Val
260 265 270

Arg Pro Val Ser Val Ala Phe Glu Val Ile Thr Gly Phe Arg Leu Tyr
275 280 285

Lys Ser Gly Val Val Thr Ser Asp His Cys Gly Thr Thr Pro Met Asp
290 295 300

Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asp Gly Val
305 310 315 320

Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly Asp Glu
325 330 335

Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Gly Val Ala Thr
340 345 350

Cys Ala Ser Tyr Pro Ile Val Ala
355 360

<210> 24
<211> 363
<212> PRT
<213> Zea mays

<400> 24

Met Ala His Arg Arg Ile Ile Leu Leu Leu Ala Val Ala Ala Val Ala
1 5 10 15

Ala Thr Ser Ala Val Ala Ala Ala Ser Ser Gly Phe Asp Asp Ser Asn
20 25 30

DMCI0099.ST25.txt

Pro Ile Arg Pro Val Thr Asp Arg Ala Ala Ser Ala Leu Glu Ser Thr
 35 40 45

Val Phe Ala Ala Leu Gly Arg Thr Arg Asp Ala Leu Arg Phe Ala Arg
 50 55 60

Phe Ala Val Arg Tyr Gly Lys Ser Tyr Glu Ser Ala Ala Glu Val His
 65 70 75 80

Lys Arg Phe Arg Ile Phe Ser Glu Ser Leu Gln Leu Val Arg Ser Thr
 85 90 95

Asn Arg Lys Gly Leu Ser Tyr Arg Leu Gly Tyr Asn Arg Phe Ala Asp
 100 105 110

Met Ser Trp Glu Glu Phe Arg Ala Thr Arg Leu Gly Ala Ala Gln Asn
 115 120 125

Cys Ser Ala Thr Leu Thr Gly Asn His Arg Met Arg Ala Ala Ala Val
 130 135 140

Ala Leu Pro Glu Thr Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro
 145 150 155 160

Val Lys Asn Gln Gly His Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr
 165 170 175

Gly Ala Leu Glu Ala Ala Tyr Thr Gln Ala Thr Gly Lys Pro Ile Ser
 180 185 190

Leu Ser Glu Gln Gln Leu Val Asp Cys Gly Phe Ala Phe Asn Asn Phe
 195 200 205

Gly Cys Asn Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Tyr
 210 215 220

Asn Gly Gly Leu Asp Thr Glu Glu Ser Tyr Pro Tyr Gln Gly Val Asn
 225 230 235 240

Gly Ile Cys Lys Phe Lys Asn Glu Asn Val Gly Val Lys Val Leu Asp
 245 250 255

Ser Val Asn Ile Thr Leu Gly Ala Glu Asp Glu Leu Lys Asp Ala Val
 260 265 270

Gly Leu Val Arg Pro Val Ser Val Ala Phe Glu Val Ile Thr Gly Phe
 275 280 285

DMCI0099.ST25.txt

Arg Leu Tyr Lys Ser Gly Val Tyr Thr Ser Asp His Cys Gly Thr Thr
 290 295 300

Pro Met Asp Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu
 305 310 315 320

Asp Gly Val Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp
 325 330 335

Gly Asp Glu Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Gly
 340 345 350

Val Ala Thr Cys Ala Ser Tyr Pro Ile Val Ala
 355 360

<210> 25
 <211> 362

<212> PRT

<213> Oryza sativa

<400> 25

Met Ala His Arg Arg Ile Ile Leu Leu Leu Ala Val Ala Ala Val Ala
 1 5 10 15

Ala Thr Ser Ala Val Ala Ala Ser Ser Gly Phe Asp Asp Ser Asn
 20 25 30

Pro Ile Arg Ser Val Thr Asp His Ala Ala Ser Ala Leu Glu Ser Thr
 35 40 45

Val Ile Ala Ala Leu Gly Arg Thr Arg Gly Ala Leu Arg Phe Ala Arg
 50 55 60

Phe Ala Val Arg Gly His Lys Arg Tyr Gly Asp Ala Ala Glu Val Gln
 65 70 75 80

Arg Arg Phe Arg Ile Phe Ser Glu Ser Leu Glu Leu Val Arg Ser Thr
 85 90 95

Asn Arg Arg Gly Leu Pro Tyr Arg Leu Gly Ile Asn Arg Phe Ala Asp
 100 105 110

Met Ser Trp Glu Glu Phe Gln Ala Ser Arg Leu Gly Ala Ala Gln Asn
 115 120 125

Cys Ser Ala Thr Leu Ala Gly Asn His Arg Met Arg Asp Ala Pro Ala
 130 135 140

Leu Pro Glu Thr Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val
 Page 18

DMCI0099.ST25.txt

145 150 155 160
Lys Asp Gln Gly His Cys Gly Ser Cys Trp Pro Phe Ser Thr Thr Gly
165 170 175

Ser Leu Glu Ala Arg Tyr Thr Gln Ala Thr Gly Pro Pro Val Ser Leu
180 185 190

Ser Glu Gln Gln Leu Ala Asp Cys Ala Thr Arg Tyr Asn Asn Phe Gly
195 200 205

Cys Ser Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Tyr Asn
210 215 220

Gly Gly Leu Asp Thr Glu Glu Ala Tyr Pro Tyr Thr Gly Val Asn Gly
225 230 235 240

Ile Cys His Tyr Lys Pro Glu Asn Ala Gly His Lys Val Leu Asp Ser
245 250 255

Val Asn Ile Thr Leu Val Ala Glu Asp Glu Leu Lys Asn Ala Val Gly
260 265 270

Leu Val Arg Pro Val Ser Val Ala Phe Gln Val Ile Asn Gly Phe Arg
275 280 285

Met Tyr Lys Ser Gly Val Tyr Thr Ser Asp His Cys Gly Thr Ser Pro
290 295 300

Met Asp Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asn
305 310 315 320

Gly Val Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly
325 330 335

Asp Asn Gly Tyr Phe Thr Met Glu Met Gly Lys Asn Met Cys Gly Ile
340 345 350

Ala Thr Cys Ala Ser Tyr Pro Ile Val Ala
355 360